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### AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning on page 35, line 29 with the following paragraph.

A1  
BLAST (Basic Local Alignment Search Tool) is a computer-automated amino acid sequence and nucleic acid sequence comparison and identification tool. The heuristic search algorithm BLAST 2.2.1 (Altschul, et al., *Nucleic Acids Res.* 25:3389, 1997; Altschul, et al., *J. Mol. Biol.* 215:403, 1990; and Madden, et al., *Meth. Enzymol.* 266:131, 1996, incorporated herein by reference) was used to search for proteins similar to the DAS5 protein sequence. The BLASTP tool (available at [www.ncbi.nih.gov/BLAST](http://www.ncbi.nih.gov/BLAST)) takes protein sequences in FASTA format, GenBank Accession numbers or GI numbers and compares them against the NCBI protein databases. ) The DAS5 sequence was queried against the non-redundant database using the standard protein-protein BLASTP version 2.2.1 (Apr-13-2001) with the following settings: matrix= BLOSUM62, gap costs: Existence: 11, Extension: 1. The % identity and % similarity (positives) measurements were determined by a pairwise blast search "BLAST 2 sequences" results version BLASTP" (Tatusova, et al., *FEMS Microbiol Lett.* 174:247, 1999, incorporated herein by reference)